CRF Errors Corrected by th STIC System Branch

Serial Numb r: 09/147,919

Batch #4/7R
6/11/99 07/12/99

CRF Processing Dat : 6/11/99
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

ENTERED
_____

☑ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☑ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: Th abov corrections must be communicated to the applicant in the first Offic Action. DO NOT send a copy of this form.

3/1/95

INPUT SET: S32192.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                  SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5        (i) APPLICANT:
 6            (A) NAME: Bavarian Nordic AS
 7            (B) STREET: Naverland 2
 8            (C) CITY: Glostrup
 9            (E) COUNTRY: Denmark
10            (F) POSTAL CODE (ZIP): 2600
11            (G) TELEPHONE: oo45 43 438 444
12
13            (A) NAME: GSF Forschungszentrum fuer Umwelt und
14                      Gesundheit GmbH
15            (B) STREET: Ingolstaedter Landstr. 1
16            (C) CITY: Neuherberg
17            (E) COUNTRY: Germany
18            (F) POSTAL CODE (ZIP): 85758
19
20      (ii) TITLE OF INVENTION: Recombinant MVA Virus Expressing Dengue Virus
21               Antigens, and The Use Thereof in Vaccines
22
23     (iii) NUMBER OF SEQUENCES: 8
24
25      (v) COMPUTER READABLE FORM:
26            (A) MEDIUM TYPE: Floppy disk
27            (B) COMPUTER: IBM PC compatible
28            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
30
31      (vi) CURRENT APPLICATION DATA:
32            (A) APPLICATION NUMBER:
33            (B) FILING DATE:
34
35     (vii) PRIOR APPLICATION DATA:
36            (A) APPLICATION NUMBER: DK 1035/96
37            (B) FILING DATE:
38
39   (2) INFORMATION FOR SEQ ID NO: 1:
40
41        (i) SEQUENCE CHARACTERISTICS:
42            (A) LENGTH: 33 base pairs
43            (B) TYPE: nucleic acid
44            (C) STRANDEDNESS: single
45            (D) TOPOLOGY: linear
46
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ENTERED

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47        (ii) MOLECULE TYPE: other nucleic acid
48             (A) DESCRIPTION:   /desc = "primer"
49
50       (iii) HYPOTHETICAL: YES
51
52        (iv) ANTI-SENSE: NO
53
54
55
56
57        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
58
59   CAGCAGGGTA CCCTCATCGT ACAGGACGTT CTC                          33
60
61   (2) INFORMATION FOR SEQ ID NO: 2:
62
63        (i) SEQUENCE CHARACTERISTICS:
64             (A) LENGTH: 42 base pairs
65             (B) TYPE: nucleic acid
66             (C) STRANDEDNESS: single
67             (D) TOPOLOGY: linear
68
69       (ii) MOLECULE TYPE: other nucleic acid
70             (A) DESCRIPTION:   /desc = "primer"
71
72
73
74
75        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
76
77   CAGCAGCCCG GGTATTCGAT GATTATTTTT AACAAAATAA CA               42
78
79   (2) INFORMATION FOR SEQ ID NO: 3:
80
81        (i) SEQUENCE CHARACTERISTICS:
82             (A) LENGTH: 36 base pairs
83             (B) TYPE: nucleic acid
84             (C) STRANDEDNESS: single
85             (D) TOPOLOGY: linear
86
87       (ii) MOLECULE TYPE: other nucleic acid
88             (A) DESCRIPTION:   /desc = "primer"
89
90       (iii) HYPOTHETICAL: YES
91
92        (iv) ANTI-SENSE: NO
93
94
95
96
97        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
98
99   CAGCAGCTGC AGGAATCATC CATTCCACTG AATAGC                      36
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100
101     (2) INFORMATION FOR SEQ ID NO: 4:
102
103         (i) SEQUENCE CHARACTERISTICS:
104             (A) LENGTH: 36 base pairs
105             (B) TYPE: nucleic acid
106             (C) STRANDEDNESS: single
107             (D) TOPOLOGY: linear
108
109         (ii) MOLECULE TYPE: other nucleic acid
110             (A) DESCRIPTION:   /desc = "primer"
111
112
113
114
115         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
116
117    CAGCAGGCAT GCCGACGAAC AAGGAACTGT AGCAGA                              36
118
119     (2) INFORMATION FOR SEQ ID NO: 5:
120
121         (i) SEQUENCE CHARACTERISTICS:
122             (A) LENGTH: 33 base pairs
123             (B) TYPE: nucleic acid
124             (C) STRANDEDNESS: single
125             (D) TOPOLOGY: linear
126
127         (ii) MOLECULE TYPE: other nucleic acid
128             (A) DESCRIPTION:   /desc = "primer"
129
130
131
132
133         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
134
135    CAGCAGGTCG ACCCCGACCG CCTTACTGCC GCC                                 33
136
137     (2) INFORMATION FOR SEQ ID NO: 6:
138
139         (i) SEQUENCE CHARACTERISTICS:
140             (A) LENGTH: 33 base pairs
141             (B) TYPE: nucleic acid
142             (C) STRANDEDNESS: single
143             (D) TOPOLOGY: linear
144
145         (ii) MOLECULE TYPE: other nucleic acid
146             (A) DESCRIPTION:   /desc = "primer"
147
148
149
150
151         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
152
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INPUT SET: S32192.raw

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153    GGGGGGCTGC AGATGGTAGC GACCGGCGCT CAG                           33
154
155    (2) INFORMATION FOR SEQ ID NO: 7:
156
157        (i) SEQUENCE CHARACTERISTICS:
158            (A) LENGTH: 36 base pairs
159            (B) TYPE: nucleic acid
160            (C) STRANDEDNESS: single
161            (D) TOPOLOGY: linear
162
163        (ii) MOLECULE TYPE: other nucleic acid
164            (A) DESCRIPTION:   /desc = "primer"
165
166
167
168
169        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
170
171    CAGCAGCCCG GGATGGCAGC AATCCTGGCA TACACC                         36
172
173    (2) INFORMATION FOR SEQ ID NO: 8:
174
175        (i) SEQUENCE CHARACTERISTICS:
176            (A) LENGTH: 39 base pairs
177            (B) TYPE: nucleic acid
178            (C) STRANDEDNESS: single
179            (D) TOPOLOGY: linear
180
181        (ii) MOLECULE TYPE: other nucleic acid
182            (A) DESCRIPTION:   /desc = "primer"
183
184
185
186
187        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
188
189    CAGCAGCCCG GGTCACTGTA GTTTGTCCAT CCTCAGCCT                       39
190
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/147,919*

INPUT SET: S32192.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Bavarian Nordic AS
7	Unknown or Misplaced Identifier	(B) STREET: Naverland 2
8	Unknown or Misplaced Identifier	(C) CITY: Glostrup
9	Unknown or Misplaced Identifier	(E) COUNTRY: Denmark
10	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 2600
11	Unknown or Misplaced Identifier	(G) TELEPHONE: oo45 43 438 444
13	Unknown or Misplaced Identifier	(A) NAME: GSF Forschungszentrum fuer Umwelt und
15	Unknown or Misplaced Identifier	(B) STREET: Ingolstaedter Landstr. 1
16	Unknown or Misplaced Identifier	(C) CITY: Neuherberg
17	Unknown or Misplaced Identifier	(E) COUNTRY: Germany
18	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 85758

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> Information Section and up to the first 5 pages.

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28                 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
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32              (A) APPLICATION NUMBER: DK 1035/96
33
34      (2) INFORMATION FOR SEQ ID NO: 1:            (vii) PRIOR APP DATA!
35
36         (i) SEQUENCE CHARACTERISTICS:
37                 (A) LENGTH: 33 base pairs
38                 (B) TYPE: nucleic acid
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47          (iv) ANTI-SENSE: NO
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54    CAGCAGGGTA CCCTCATCGT ACAGGACGTT CTC                              33
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72    CAGCAGCCCG GGTATTCGAT GATTATTTTT AACAAAATAA CA                    42
73
74    (2) INFORMATION FOR SEQ ID NO: 3:
75
76          (i) SEQUENCE CHARACTERISTICS:
77              (A) LENGTH: 36 base pairs
78              (B) TYPE: nucleic acid
79              (C) STRANDEDNESS: single
80              (D) TOPOLOGY: linear
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82         (ii) MOLECULE TYPE: other nucleic acid
83              (A) DESCRIPTION:   /desc = "primer"
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85        (iii) HYPOTHETICAL: YES
86
87         (iv) ANTI-SENSE: NO
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92          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
93
94    CAGCAGCTGC AGGAATCATC CATTCCACTG AATAGC                          36
95
96    (2) INFORMATION FOR SEQ ID NO: 4:
97
98          (i) SEQUENCE CHARACTERISTICS:
99              (A) LENGTH: 36 base pairs
```

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100              (B) TYPE: nucleic acid
101              (C) STRANDEDNESS: single
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136              (B) TYPE: nucleic acid
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138              (D) TOPOLOGY: linear
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141              (A) DESCRIPTION:   /desc = "primer"
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143
144
145
146        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
147
148   GGGGGGCTGC AGATGGTAGC GACCGGCGCT CAG                       33
149
150   (2) INFORMATION FOR SEQ ID NO: 7:
151
152        (i) SEQUENCE CHARACTERISTICS:
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153              (A) LENGTH: 36 base pairs
154              (B) TYPE: nucleic acid
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156              (D) TOPOLOGY: linear
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182        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
183
184   CAGCAGCCCG GGTCACTGTA GTTTGTCCAT CCTCAGCCT                         39
185
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/147,919*

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